

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hunter, Shirley Wu
Sim, Gek-Kee
Weber, Eric R.

(ii) TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS

(iii) NUMBER OF SEQUENCES: 88

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SHERIDAN ROSS P.C.
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(E) COUNTRY: U.S.A.
(F) ZIP: 80202

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/171,156
(B) FILING DATE: 1998-10-09
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Connell, Gary J.
(B) REGISTRATION NUMBER: 32,020
(C) REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 303/863-9700
(B) TELEFAX: 303/863-0223

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Arg Gly Asn His Val Phe Leu Glu Asp Gly Met Ala Asp Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Xaa = Tyr or Asp
(B) LOCATION: 5

(ix) FEATURE:

(A) NAME/KEY: Xaa = any amino acid
(B) LOCATION: 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Tyr Arg Asn Xaa Xaa Thr Asn Asp Pro Gln Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu Ile Lys Arg Asn Asp Arg Glu Pro Gly Asn Leu Ser Lys Ile Arg
1 5 10 15

Thr Val Met Asp Lys Val Ile Lys Gln Thr Gln
20 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Xaa = Ala or His
(B) LOCATION: 8

(ix) FEATURE:

(A) NAME/KEY: Xaa = Ala or His
(B) LOCATION: 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Lys Asp Asn Asp Ile Tyr Xaa Xaa Arg Asp Ile Asn Glu Ile Leu
1 5 10 15

Arg Val Leu Asp Pro Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Xaa = any amino acid
 - (B) LOCATION: 12
- (ix) FEATURE:
 - (A) NAME/KEY: Xaa = any amino acid
 - (B) LOCATION: 18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Tyr Gly Arg Val Gln Ile Glu Asp Tyr Thr Xaa Ser Asn His Lys
1 5 10 15

Asp Xaa Glu Glu Lys Asp Gln Ile Asn Gly Leu
20 25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Xaa = any amino acid
 - (B) LOCATION: 5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Tyr Arg Asn Xaa Tyr Thr Asn Asp Pro Gln Leu Lys Leu Leu Asp
1 5 10 15

Glu Gly

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Xaa = any amino acid
(B) LOCATION: 13

(ix) FEATURE:
(A) NAME/KEY: Xaa = any amino acid
(B) LOCATION: 19

(ix) FEATURE:
(A) NAME/KEY: Xaa = any amino acid
(B) LOCATION: 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr Phe Asn Asp Gln Ile Lys Ser Val Met Glu Pro Xaa Val Phe Lys
1 5 10 15
Tyr Pro Xaa Ala Xaa Leu
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGRTTTCCWA TRAARTCTTC 20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA CGAGTGAAT TCAATATTTT GTTTTACATT AAATTTTCA AATTCGATAT	60
GAAATTTTA CTGGCAATT GCGTGTGTG TGTTTTATTA AATCAAGTAT CTATGTAAA	120
AATGGTCACT GAAAAGTGTG AGTCAGGTGG AAATAATCCA AGTACAGAAG AGGTGTCAAT	180
ACCATCTGGG AAGCTTACTA TTGAAGATTT TTGTATTGGA AATCA	225

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTCGGCAC GAGTG

15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 45..314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAAATTCAA TATTTGTTT TACATTAAT TTTTCAAATT CGAT ATG AAA TTT TTA
Met Lys Phe Leu
1

56

CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA GTA TCT ATG TCA
Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln Val Ser Met Ser
5 10 15 20

104

AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT AAT CCA AGT ACA
Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser Thr
25 30 35

152

GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT TGT
Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe Cys
40 45 50

200

ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA AGT CAA TGT GGA
Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys Ser Gln Cys Gly
55 60 65

248

TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT CAA
Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr Arg Pro Asn Gln
70 75 80

296

AAA CAC TGT TAT TGC GAA TAACCATATT CCGGATGAAA GACCAAATTG
Lys His Cys Tyr Cys Glu
85 90

344

ATATAAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC	404
CTAACATGTT TTGCCTCCAA TTTATTTAA CAGCAAATTG CTGGAACCTTA CCGTACCGTA	464
ACTAAATGTT CAAGAAATAC TGAATGTTA CAAATAGATT ATTATAAATA TTGTAACATT	524
GTCTAATATT TATAAGAATT ATATAAACTG AATTGCAAAA A	565

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln	
1 5 10 15	
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn	
20 25 30	
Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile	
35 40 45	
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys	
50 55 60	
Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr	
65 70 75 80	
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu	
85 90	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT AAT CAA	48
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Asn Gln	
1 5 10 15	
GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT	96
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn	
20 25 30	

AAT CCA AGT ACA GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile 35 40 45	144
GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys 50 55 60	192
AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr 65 70 75 80	240
CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA Arg Pro Asn Gln Lys His Cys Tyr Cys Glu 85 90	270

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln 1 5 10 15
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn 20 25 30
Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile 35 40 45
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys 50 55 60
Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr 65 70 75 80
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu 85 90

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..26
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTGGATCCG TCAAAATGG TCACTG

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGGAATTCTG GTTATTCGCA ATAACAGT

28

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGAAATCTC CTATCACAGT GTACGGAGTG TAAAATATTG TTGAAGTATT TTGAAATTAA

60

TTAATTATT CGAAAAGGAG ATTCATTAATAAAAATG GTT TAC GAA AGT GAC
Met Val Tyr Ser Asp

1 5

TTT TAC ACG ACC CGT CGG CCC TAC AGT CGT CCG GCT TTG TCT TCA TAC
Phe Tyr Thr Arg Arg Pro Tyr Ser Arg Pro Ala Leu Ser Ser Tyr

10 15 20

TCC GTA ACG GCA CGT CCA GAG CCG GTT CCT TGG GAC AAA TTG CCG TTC
Ser Val Thr Ala Arg Pro Glu Pro Val Pro Trp Asp Lys Leu Pro Phe

25 30 35

GTC CCC CGT CCA AGT TTG GTA GCA GAT CCC ATA ACA GCA TTT TGC AAG
Val Pro Arg Pro Ser Leu Val Ala Asp Pro Ile Thr Ala Phe Cys Lys

40 45 50

CGA AAA CCT CGC CGA GAA GAA GTT CAA AAA GAG TCC ATT GTT CGA
Arg Lys Pro Arg Arg Glu Glu Val Val Gln Lys Glu Ser Ile Val Arg

55 60 65 70

258

306

42074232 02020202

AGG ATC AAT TCT GCA GGA ATT AAA CCC AGC CAG AGA GTT TTA TCG GCT	354																																																				
Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser Gln Arg Val Leu Ser Ala																																																					
75	80		85	CCA ATA AGA GAA TAC GAA TCC CCA AGG GAC CAG ACC AGG CGT AAA GTT	402	Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp Gln Thr Arg Arg Lys Val		90	95		100	TTG GAA AGC GTC AGA AGA CAA GAA GCT TTT CTG AAC CAA GGA GGA ATT	450	Leu Glu Ser Val Arg Arg Gln Glu Ala Phe Leu Asn Gln Gly Gly Ile		105	110		115	TGT CCA TTG ACC ACC AGA AAT GAT GAC ATG GAT AGA CTT CTA CCC CGT	498	Cys Pro Leu Thr Thr Arg Asn Asp Asp Met Asp Arg Leu Leu Pro Arg		120	125		130	CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG	546	Leu His Ser Ser His Thr Thr Pro Ser Ala Asp Arg Lys Val Leu Leu		135	140		145		150	ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG	598	Thr Thr Phe His Arg Arg Tyr		155		AAGTCATGTG GTGTTTTTA TACATTCTT ATTAAATCGAT ATTCCCTAACG AACGATACGA	658	TAACCTTCGA TAACTTTTC TGTTTAATT TGACAAAATA TGCATTTGCA AGCATAACAT	718	TCATTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTAA AAAGTGTGGA AACAAAGCGTA	778	GTGTTAACAA ATGCATTGCT TGTTTGATT ATTTATTAT CTATTATATA TTCCATATTG	838	TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAA	897
	85																																																				
CCA ATA AGA GAA TAC GAA TCC CCA AGG GAC CAG ACC AGG CGT AAA GTT	402																																																				
Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp Gln Thr Arg Arg Lys Val																																																					
90	95		100	TTG GAA AGC GTC AGA AGA CAA GAA GCT TTT CTG AAC CAA GGA GGA ATT	450	Leu Glu Ser Val Arg Arg Gln Glu Ala Phe Leu Asn Gln Gly Gly Ile		105	110		115	TGT CCA TTG ACC ACC AGA AAT GAT GAC ATG GAT AGA CTT CTA CCC CGT	498	Cys Pro Leu Thr Thr Arg Asn Asp Asp Met Asp Arg Leu Leu Pro Arg		120	125		130	CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG	546	Leu His Ser Ser His Thr Thr Pro Ser Ala Asp Arg Lys Val Leu Leu		135	140		145		150	ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG	598	Thr Thr Phe His Arg Arg Tyr		155		AAGTCATGTG GTGTTTTTA TACATTCTT ATTAAATCGAT ATTCCCTAACG AACGATACGA	658	TAACCTTCGA TAACTTTTC TGTTTAATT TGACAAAATA TGCATTTGCA AGCATAACAT	718	TCATTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTAA AAAGTGTGGA AACAAAGCGTA	778	GTGTTAACAA ATGCATTGCT TGTTTGATT ATTTATTAT CTATTATATA TTCCATATTG	838	TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAA	897								
	100																																																				
TTG GAA AGC GTC AGA AGA CAA GAA GCT TTT CTG AAC CAA GGA GGA ATT	450																																																				
Leu Glu Ser Val Arg Arg Gln Glu Ala Phe Leu Asn Gln Gly Gly Ile																																																					
105	110		115	TGT CCA TTG ACC ACC AGA AAT GAT GAC ATG GAT AGA CTT CTA CCC CGT	498	Cys Pro Leu Thr Thr Arg Asn Asp Asp Met Asp Arg Leu Leu Pro Arg		120	125		130	CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG	546	Leu His Ser Ser His Thr Thr Pro Ser Ala Asp Arg Lys Val Leu Leu		135	140		145		150	ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG	598	Thr Thr Phe His Arg Arg Tyr		155		AAGTCATGTG GTGTTTTTA TACATTCTT ATTAAATCGAT ATTCCCTAACG AACGATACGA	658	TAACCTTCGA TAACTTTTC TGTTTAATT TGACAAAATA TGCATTTGCA AGCATAACAT	718	TCATTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTAA AAAGTGTGGA AACAAAGCGTA	778	GTGTTAACAA ATGCATTGCT TGTTTGATT ATTTATTAT CTATTATATA TTCCATATTG	838	TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAA	897																
	115																																																				
TGT CCA TTG ACC ACC AGA AAT GAT GAC ATG GAT AGA CTT CTA CCC CGT	498																																																				
Cys Pro Leu Thr Thr Arg Asn Asp Asp Met Asp Arg Leu Leu Pro Arg																																																					
120	125		130	CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG	546	Leu His Ser Ser His Thr Thr Pro Ser Ala Asp Arg Lys Val Leu Leu		135	140		145		150	ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG	598	Thr Thr Phe His Arg Arg Tyr		155		AAGTCATGTG GTGTTTTTA TACATTCTT ATTAAATCGAT ATTCCCTAACG AACGATACGA	658	TAACCTTCGA TAACTTTTC TGTTTAATT TGACAAAATA TGCATTTGCA AGCATAACAT	718	TCATTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTAA AAAGTGTGGA AACAAAGCGTA	778	GTGTTAACAA ATGCATTGCT TGTTTGATT ATTTATTAT CTATTATATA TTCCATATTG	838	TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAA	897																								
	130																																																				
CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG	546																																																				
Leu His Ser Ser His Thr Thr Pro Ser Ala Asp Arg Lys Val Leu Leu																																																					
135	140		145		150	ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG	598	Thr Thr Phe His Arg Arg Tyr		155		AAGTCATGTG GTGTTTTTA TACATTCTT ATTAAATCGAT ATTCCCTAACG AACGATACGA	658	TAACCTTCGA TAACTTTTC TGTTTAATT TGACAAAATA TGCATTTGCA AGCATAACAT	718	TCATTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTAA AAAGTGTGGA AACAAAGCGTA	778	GTGTTAACAA ATGCATTGCT TGTTTGATT ATTTATTAT CTATTATATA TTCCATATTG	838	TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAA	897																																
	145		150	ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG	598	Thr Thr Phe His Arg Arg Tyr		155		AAGTCATGTG GTGTTTTTA TACATTCTT ATTAAATCGAT ATTCCCTAACG AACGATACGA	658	TAACCTTCGA TAACTTTTC TGTTTAATT TGACAAAATA TGCATTTGCA AGCATAACAT	718	TCATTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTAA AAAGTGTGGA AACAAAGCGTA	778	GTGTTAACAA ATGCATTGCT TGTTTGATT ATTTATTAT CTATTATATA TTCCATATTG	838	TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAA	897																																		
	150																																																				
ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG	598																																																				
Thr Thr Phe His Arg Arg Tyr																																																					
155																																																					
AAGTCATGTG GTGTTTTTA TACATTCTT ATTAAATCGAT ATTCCCTAACG AACGATACGA	658																																																				
TAACCTTCGA TAACTTTTC TGTTTAATT TGACAAAATA TGCATTTGCA AGCATAACAT	718																																																				
TCATTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTAA AAAGTGTGGA AACAAAGCGTA	778																																																				
GTGTTAACAA ATGCATTGCT TGTTTGATT ATTTATTAT CTATTATATA TTCCATATTG	838																																																				
TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAA	897																																																				

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Val Tyr Glu Ser Asp Phe Tyr Thr Thr Arg Arg Pro Tyr Ser Arg			
1	5	10	15
Pro Ala Leu Ser Ser Tyr Ser Val Thr Ala Arg Pro Glu Pro Val Pro			
20	25	30	
Trp Asp Lys Leu Pro Phe Val Pro Arg Pro Ser Leu Val Ala Asp Pro			
35	40	45	
Ile Thr Ala Phe Cys Lys Arg Lys Pro Arg Arg Glu Glu Val Val Gln			
50	55	60	
Lys Glu Ser Ile Val Arg Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser			
65	70	75	80
Gln Arg Val Leu Ser Ala Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp			

85

90

95

Gln Thr Arg Arg Lys Val Leu Glu Ser Val Arg Arg Gln Glu Ala Phe
 100 105 110

Leu Asn Gln Gly Gly Ile Cys Pro Leu Thr Thr Arg Asn Asp Asp Met
 115 120 125

Asp Arg Leu Leu Pro Arg Leu His Ser Ser His Thr Thr Pro Ser Ala
 130 135 140

Asp Arg Lys Val Leu Leu Thr Thr Phe His Arg Arg Tyr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGGTTTACG AAAGTGACTT TTACACGACC CGTCGGCCCT ACAGTCGTCC GGCTTTGTCT	60
TCATACTCCG TAACGGCACG TCCAGAGCCG GTTCCTTGGG ACAAAATTGCC GTTCGTCCCC	120
CGTCCAAGTT TGGTAGCAGA TCCCATAACA GCATTTGCA AGCGAAAACC TCGCCGAGAA	180
GAAGTTGTTCA AAAAAGAGTC CATTGTTCGA AGGATCAATT CTGCAGGAAT TAAACCCAGC	240
CAGAGAGTTT TATCGGCTCC AATAAGAGAA TACGAATCCC CAAGGGACCA GACCAGGCCT	300
AAAGTTTGG AAAGCGTCAG AAGACAAGAA GCTTTCTGA ACCAAGGAGG AATTGTCCA	360
TTGACCACCA GAAATGATGA CATGGATAGA CTTCTACCCC GTCTCCACAG TTCACACACA	420
ACACCTTCTG CGGATAGGAA AGTTTGTG ACCACTTTC ACAGAAGATA C	471

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5..2706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GC GG ATG AAG AGC ATC GAG GCT TAT ACA AAC AGA TAT GAA ATC ATA GCT	49
Met Lys Ser Ile Glu Ala Tyr Thr Asn Arg Tyr Glu Ile Ile Ala	
1 5 10 15	

TCT GAA ATA GTT AAT CTT CGA ATG AAA CCA GAT GAT TTT AAT TTA ATA	97
Ser Glu Ile Val Asn Leu Arg Met Lys Pro Asp Asp Phe Asn Leu Ile	
20 25 30	
AAA GTT ATT GGT CGA GGA GCA TTT GGT GAA GTA CAG TTA GTG CGA CAC	145
Lys Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His	
35 40 45	
AAA TCA ACT GCA CAA GTT TTT GCT ATG AAA CGC CTA TCA AAA TTT GAA	193
Lys Ser Thr Ala Gln Val Phe Ala Met Lys Arg Leu Ser Lys Phe Glu	
50 55 60	
ATG ATT AAG AGA CCA GAC TCT GCA TTT TTT TGG GAA GAA CGT CAT ATA	241
Met Ile Lys Arg Pro Asp Ser Ala Phe Phe Trp Glu Glu Arg His Ile	
65 70 75	
ATG GCT CAT GCA AAA TCA GAA TGG ATT GTA CAA TTA CAT TTT GCT TTT	289
Met Ala His Ala Lys Ser Glu Trp Ile Val Gln Leu His Phe Ala Phe	
80 85 90 95	
CAA GAT CAA AAA TAT CTT TAT ATG GTC ATG GAT TAT ATG CCG GGG GGT	337
Gln Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly	
100 105 110	
GAC TTG GTG AGT CTT ATG TCC GAT TAT GAA ATT CCA GAA AAA TGG GCA	385
Asp Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala	
115 120 125	
ATG TTC TAT ACA ATG GAA GTG GTG CTA GCA CTT GAT ACA ATT CAC TCC	433
Met Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser	
130 135 140	
ATG GGA TTT GTA CAT CGT GAT GTT AAA CCT GAT AAT ATG CTT CTA GAC	481
Met Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp	
145 150 155	
AAA TAT GGT CAT TTA AAG TTA GCT GAC TTT GGA ACC TGT ATG AAA ATG	529
Lys Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met	
160 165 170 175	
GAT ACA GAT GGT TTG GTA CGT TCT AAT GCT GTT GGA ACG CCT GAT	577
Asp Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp	
180 185 190	
TAC ATT TCT CCC GAA GTT TTG CAG TCC CAA GGT GGT GAA GGA GTT TAC	625
Tyr Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Glu Gly Val Tyr	
195 200 205	
GGT CGT GAA TGC GAT TGG TGG TCT GTG GGA ATT TTT TTG TAT GAA ATG	673
Gly Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met	
210 215 220	
TTA TTT GGA GAA ACA CCT TTT TAT GCA GAC AGT TTG GTT GGA ACT TAC	721
Leu Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr	
225 230 235	
AGT AAA ATT ATG GAT CAC AGA AAC TCA TTA ACT TTT CCT CCA GAA GTG	769
Ser Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val	
240 245 250 255	

GAA ATA AGC CAA TAT GCC CGA TCT TTG ATA CAA GGA TTT TTA ACA GAC 817
 Glu Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp
 260 265 270

 AGA ACA CAG CGT TTA GGC AGA AAT GAA GTG GAA GAA ATT AAA CGA CAT 865
 Arg Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Glu Ile Lys Arg His
 275 280 285

 CCA TTT TTC ATA AAT GAT CAA TGG ACT TTT GAC AAT TTA AGA GAC TCT 913
 Pro Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser
 290 295 300

 GCC CCA CCT GTA GTG CCA GAG CTG AGT GGT GAT GAT GAT ACA AGG AAC 961
 Ala Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn
 305 310 315

 TTT GAT GAT ATT GAA CGT GAT GAA ACA CCT GAA GAG AAT TTT CCT ATA 1009
 Phe Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile
 320 325 330 335

 CCA AAA ACT TTT GCT GGT AAT CAT CTG CCA TTT GTT GGA TTC ACA TAT 1057
 Pro Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr
 340 345 350

 AAT GGT GAT TAC CAA TTA TTA ACA AAT GGA GGT GTT AGA AAT AGT GAT 1105
 Asn Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp
 355 360 365

 ATG GTT GAT ACA AAA TTA AAC AAC ATT TGT GTT TCA AGT AAG GAT GAT 1153
 Met Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp
 370 375 380

 GTG TTA AAT TTA CAA AAT TTA GAA CAA GAG AAA GGT AAC AGT GAA 1201
 Val Leu Asn Leu Gln Asn Leu Glu Gln Glu Lys Gly Asn Ser Glu
 385 390 395

 AAT TTG AAA ACA AAC ACC CAA TTA AGT AAT AAA TTA GAT GAA CTA 1249
 Asn Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu
 400 405 410 415

 GGT CAG AGA GAA TGT GAA TTA AGG AAT CAG GCT GGA GAT TAT GAG AAA 1297
 Gly Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys
 420 425 430

 GAA TTG ACT AAA TTC AAA TTA TCG TGC AAA GAA TTA CAA CGT AAG GCA 1345
 Glu Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala
 435 440 445

 GAA TTT GAG AAT GAA TTA CGG CGT AAA ACT GAG TCC TTA CTA GTT GAA 1393
 Glu Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu
 450 455 460

 ACA AAG AAA AGA CTA GAC GAA GAG CAG AAT AAA AGA ACT AGA GAA ATG 1441
 Thr Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met
 465 470 475

 AAT AAT AAT CAA CAG CAC AAT GAC AAA ATA AAT ATG TTA GAA AAA CAA 1489
 Asn Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln
 480 485 490 495

 ATT AAT GAT TTA CAA GAA AAA TTG AAA GGT GAA TTA GAG CAC AAT CAG 1537

Ile Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln			
500	505	510	
AAA TTA AAG AAG CAA GCT GTT GAG CTT AGA GTT GCT CAG TCT GCT ACT			1585
Lys Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr			
515	520	525	
GAA CAA CTG AAT AAT GAA TTA CAG GAA ACT ATG CAG GGT TTA CAA ACA			1633
Glu Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr			
530	535	540	
CAA AGA GAT GCT TTA CAA CAA GAA GTA GCA TCT CTC CAA GGC AAA CTT			1681
Gln Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu			
545	550	555	
TCT CAA GAG AGG AGC TCT AGA TCA CAG GCT TCT GAT ATG CAG ATA GAA			1729
Ser Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu			
560	565	570	575
CTA GAA GCA AAA TTG CAG GCT CTC CAT ATT GAA CTG GAG CAT GTC AGA			1777
Leu Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg			
580	585	590	
AAT TGT GAA GAC AAA GTT ACC CAA GAC AAC AGA CAA CTA TTG GAA AGG			1825
Asn Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg			
595	600	605	
ATA TCA ACA TTG GAG AAA GAA TGT GCT TCT CTA GAA TTA GAA TTG AAA			1873
Ile Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys			
610	615	620	
GCA ACA CAA AAC AAA TAT GAG CAA GAG GTC AAA GCA CAT CGC GAA ACT			1921
Ala Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr			
625	630	635	
GAA AAA TCA AGA CTG GTC AGT AAA GAA GAA GCA AAT ATG GAG GAA GTT			1969
Glu Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val			
640	645	650	655
AAA GCA CTC CAA ATA AAA TTA AAT GAA GAG AAA TCT GCT CGA CAG AAA			2017
Lys Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys			
660	665	670	
TCT GAT CAG AAT TCT CAA GAA AAG GAA CGA CAA ATT TCT ATG TTA TCT			2065
Ser Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser			
675	680	685	
GTG GAT TAT CGT CAA ATC CAA CAG CGT TTG CAA AAG CTA GAA GGA GAA			2113
Val Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu			
690	695	700	
TAT AGG CAA GAG AGT GAA AAA GTT AAA GCT CTC CAC AGT CAG ATT GAG			2161
Tyr Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu			
705	710	715	
CAA GAG CAA CTA AAA AAA TCA CAA TTA CAA AGC GAA TTG GGT GTT CAA			2209
Gln Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln			
720	725	730	735
AGG TCT CAG ACT GCA CAT TTA ACA GCC AGG GAA GCT CAG CTA GTT GGA			2257
Arg Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly			

740	745	750	
GAA GTT GCT CAT CTT AGA GAT GCT AAA AGA AAT GTT GAA GAA GAG TTA Glu Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Leu 755	760	765	2305
CAC AAG TTA AAA ACT GCT CGA TCA GTG GAT AAT GCT CAG ATG AAA GAG His Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu 770	775	780	2353
CTT CAA GAA CAA GTT GAA GCC GAG CAA GTT TTC TCG ACT CTT TAT AAA Leu Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys 785	790	795	2401
ACA CAT TCT AAT GAA CTT AAG GAA GAA CTT GAG GAA AAA TCT CGT CAT Thr His Ser Asn Glu Leu Lys Glu Glu Leu Glu Lys Ser Arg His 800	805	810	2449
ATT CAA GAA ATG GAA GAA GAA AGA GAA AGT TTG GTT CAT CAG CTA CAA Ile Gln Glu Met Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln 820	825	830	2497
ATT GCA TTA GCT AGA GCT GAT TCA GAG GCA TTG GCG AGA TCA ATA GCT Ile Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala 835	840	845	2545
GAT GAA AGT ATA GCT GAT TTA GAA AAG GAA AAG ACT ATG AAG GAA TTA Asp Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu 850	855	860	2593
GAA CTA AAA GAA TTA TTA AAC AAA AAT CGT ACT GAA CTT TCC CAG AAA Glu Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys 865	870	875	2641
GAC ATT TCA ATA AGT GCA TTG CGT GAA CGA GAA AAT GAA CAG AAG AAA Asp Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys 880	885	890	2689
CTT TTA GAA CAA ATC TC Leu Leu Glu Gln Ile 900			2706

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Lys	Ser	Ile	Glu	Ala	Tyr	Thr	Asn	Arg	Tyr	Glu	Ile	Ile	Ala	Ser
1			5				10						15		
Glu	Ile	Val	Asn	Leu	Arg	Met	Lys	Pro	Asp	Asp	Phe	Asn	Leu	Ile	Lys
						20		25			30				
Val	Ile	Gly	Arg	Gly	Ala	Phe	Gly	Glu	Val	Gln	Leu	Val	Arg	His	Lys
						35		40			45				

Ser Thr Ala Gln Val Phe Ala Met Lys Arg Leu Ser Lys Phe Glu Met
 50 55 60
 Ile Lys Arg Pro Asp Ser Ala Phe Phe Trp Glu Glu Arg His Ile Met
 65 70 75 80
 Ala His Ala Lys Ser Glu Trp Ile Val Gln Leu His Phe Ala Phe Gln
 85 90 95
 Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly Asp
 100 105 110
 Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala Met
 115 120 125
 Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser Met
 130 135 140
 Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
 145 150 155 160
 Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asp
 165 170 175
 Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp Tyr
 180 185 190
 Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Gly Glu Gly Val Tyr Gly
 195 200 205
 Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met Leu
 210 215 220
 Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
 225 230 235 240
 Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val Glu
 245 250 255
 Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp Arg
 260 265 270
 Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Glu Ile Lys Arg His Pro
 275 280 285
 Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser Ala
 290 295 300
 Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn Phe
 305 310 315 320
 Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile Pro
 325 330 335
 Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr Asn
 340 345 350
 Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp Met
 355 360 365

Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp Val
370 375 380

Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu Asn
385 390 395 400

Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu Gly
405 410 415

Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys Glu
420 425 430

Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala Glu
435 440 445

Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu Thr
450 455 460

Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met Asn
465 470 475 480

Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln Ile
485 490 495

Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln Lys
500 505 510

Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr Glu
515 520 525

Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr Gln
530 535 540

Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu Ser
545 550 555 560

Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu Leu
565 570 575

Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg Asn
580 585 590

Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Glu Arg Ile
595 600 605

Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys Ala
610 615 620

Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr Glu
625 630 635 640

Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val Lys
645 650 655

Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys Ser
660 665 670

Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser Val
675 680 685

Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu Tyr

690

695

700

Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu Gln
 705 710 715 720

Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln Arg
 725 730 735

Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly Glu
 740 745 750

Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Glu Leu His
 755 760 765

Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu Leu
 770 775 780

Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys Thr
 785 790 795 800

His Ser Asn Glu Leu Lys Glu Glu Leu Glu Glu Lys Ser Arg His Ile
 805 810 815

Gln Glu Met Glu Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln Ile
 820 825 830

Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala Asp
 835 840 845

Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu Glu
 850 855 860

Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys Asp
 865 870 875 880

Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys Leu
 885 890 895

Leu Glu Gln Ile
 900

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GA GCT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA
 Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly
 1 5 10 15

47

AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr 20 25 30	95
GAT GAG AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val 35 40 45	143
ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu 50 55 60	191
AAT GGA AAT GTG ATT AGC ATT ACT GAT GAG AAT GGA AAT GTG ATT AGC Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser 65 70 75	239
ATT ACT GAT GAA AAT GGA AAC TCG AAT AGC ACT ACT AGT GTT TTC AAT Ile Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn 80 85 90 95	287
GAA ACT GAA AAT ATG ACT GGT GCT GCT GAT ACA AAT GAA TAT TCA ATT Glu Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile 100 105 110	335
GGT TCT ACT GAC GGA AAT GGA AAT TTT ATA AGT ACT TTT AGT GAT CAT Gly Ser Thr Asp Gly Asn Phe Ile Ser Thr Phe Ser Asp His 115 120 125	383
GAT TAC GTA AGT AAT ACT GAA GAA AAT GAA A Asp Tyr Val Ser Asn Thr Glu Glu Asn Glu 130 135	414

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn 1 5 10 15	
Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp 20 25 30	
Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile 35 40 45	
Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn 50 55 60	
Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser Ile 65 70 75 80	
Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn Glu 85 90 95	

Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile Gly
 100 105 110
 Ser Thr Asp Gly Asn Gly Asn Phe Ile Ser Thr Phe Ser Asp His Asp
 115 120 125
 Tyr Val Ser Asn Thr Glu Glu Asn Glu
 130 135

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AT GAG AAT CGA AAT GTG ATT AGC TAT ACT GAT GAA AAT GGA AAC ATT Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile 1 5 10 15	47
ATC AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu 20 25 30	95
AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATC AGT Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser 35 40 45	143
ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly 50 55 60	191
AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr 65 70 75	239
GAT GAG AAT GGA AAT GTG ATT AGC AAT ACT CGA G Asp Glu Asn Gly Asn Val Ile Ser Asn Thr Arg 80 85 90	273

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile Ile
 1 5 10 15
 Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn
 20 25 30
 Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr
 35 40 45
 Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn
 50 55 60
 Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp
 65 70 75 80
 Glu Asn Gly Asn Val Ile Ser Asn Thr Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 24..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGAAACCCG ACATTCTCAA AAT ATG GAA CCT CAA TCG CTG TCT TGG CAA	50
Met Glu Pro Gln Ser Leu Ser Trp Gln	
1 5	
CTT CCG ACT CAA GTA GTT CAG CCA GTT TTT GAA CAA CAA ATG CAG ATT	98
Leu Pro Thr Gln Val Val Gln Pro Val Phe Glu Gln Gln Met Gln Ile	
10 15 20 25	
CCT GGA TAT ATG CAA ATT CAA TCT AAT TAT TAT CAA ATT CAC CCA	146
Pro Gly Tyr Asn Met Gln Ile Gln Ser Asn Tyr Tyr Gln Ile His Pro	
30 35 40	
GAA ATG TTG GAT CCA AAT TTG AAC AAT CCT CAG CAG TTA ATG TTT AAT	194
Glu Met Leu Asp Pro Asn Leu Asn Asn Pro Gln Gln Leu Met Phe Asn	
45 50 55	
TAT ATG CAA TTA CAA CAA TTG TCA GAA CTA CAA CAT TTA AGT CAA CAA	242
Tyr Met Gln Leu Gln Gln Leu Gln Glu Leu Gln His Leu Ser Gln Gln	
60 65 70	
CAG CCA ATG CAT CAT GAA TTT GAA CAT CAT ATC CCC ATT CCA CAA GAA	290
Gln Pro Met His His Glu Phe Glu His His Ile Pro Ile Pro Gln Glu	
75 80 85	
GCA ACT TCA ACT AAT TAC GGT CCA TCC GGA CAG TAT ATT ACT AGT GAC	338
Ala Thr Ser Thr Asn Tyr Gly Pro Ser Gly Gln Tyr Ile Thr Ser Asp	
90 95 100 105	

GCA ACA TCT TAT CAA TCA ATT GCC CAA CAA TTT GTA CCA CAA CCA CCA 386
 Ala Thr Ser Tyr Gln Ser Ile Ala Gln Gln Phe Val Pro Gln Pro Pro
 110 115 120

ATT GAA ACT ACC ACC ACG AAA ATA CCT GAA ACT GAA ATT CAA ATT GGC 434
 Ile Glu Thr Thr Thr Lys Ile Pro Glu Thr Glu Ile Gln Ile Gly
 125 130 135

GTT TCG AAT CAA TAT GCC CAA AAT ATA ACT TAT AAT TCA AAT ATC AGT 482
 Val Ser Asn Gln Tyr Ala Gln Asn Ile Thr Tyr Asn Ser Asn Ile Ser
 140 145 150

CCT GAA GTG ATT GGA TTC CGA GAA CAT TAT GTT GCG GAA CAG CCT TCT 530
 Pro Glu Val Ile Gly Phe Arg Glu His Tyr Val Ala Glu Gln Pro Ser
 155 160 165

GGT GAC GTG CTT CAC AAA AGT CAT TTA ACA GAA CAA CCA GCA GAT AAA 578
 Gly Asp Val Leu His Lys Ser His Leu Thr Glu Gln Pro Ala Asp Lys
 170 175 180 185

AGC ACA CGT GGT GAT CAG GAA CCT GTT AGT GAG ACA GGC TCT GGT TTT 626
 Ser Thr Arg Gly Asp Gln Glu Pro Val Ser Glu Thr Gly Ser Gly Phe
 190 195 200

TCG TAT GCA CAA ATT TTA TCA CAG GGA CTT AAG CCT ACC CAG CCA TCC 674
 Ser Tyr Ala Gln Ile Leu Ser Gln Gly Leu Lys Pro Thr Gln Pro Ser
 205 210 215

AAC TCA GTT AAT TTG CTT GCA GAT CGA TCG AGA TCA CCT CTA GAT ACG 722
 Asn Ser Val Asn Leu Leu Ala Asp Arg Ser Arg Ser Pro Leu Asp Thr
 220 225 230

AAA ACG AAA GAA AAT TAT AAA TCT CCT GGT CGT GTG CAG GAT ATC ACG 770
 Lys Thr Lys Glu Asn Tyr Lys Ser Pro Gly Arg Val Gln Asp Ile Thr
 235 240 245

AAA ATA ATA GAT GAG AAA CAA AAG TCG TCA AAA GAC ACA GAG TGG CAT 818
 Lys Ile Ile Asp Glu Lys Gln Lys Ser Ser Lys Asp Thr Glu Trp His
 250 255 260 265

AAT AAG AAA GTG AAA GAA CAT AAA AAA GTG AAA GAT ATC AAA CCT GAT 866
 Asn Lys Lys Val Lys Glu His Lys Val Lys Asp Ile Lys Pro Asp
 270 275 280

TTC GAA TCT TCT CAA AGG AAT AAG AAA AGC AAG AAT ATT CCT AAG CAA 914
 Phe Glu Ser Ser Gln Arg Asn Lys Ser Lys Asn Ile Pro Lys Gln
 285 290 295

ATT GAA AAT ATC ACA CCT CAA CTT GAC AGC TTA CGA TCA CGA GAT ATA 962
 Ile Glu Asn Ile Thr Pro Gln Leu Asp Ser Leu Arg Ser Arg Asp Ile
 300 305 310

GTA ATT AAG GGA GAA TTA CTA ACA AAA GAT ACT ACA AAA AGT TTA ACT 1010
 Val Ile Lys Gly Glu Leu Leu Thr Lys Asp Thr Thr Lys Ser Leu Thr
 315 320 325

ACT GTT AAT GTT GAT AGT GAA TTA GAT AGT GTA AAA CCT AAA GAT GAA 1058
 Thr Val Asn Val Asp Ser Glu Leu Asp Ser Val Lys Pro Lys Asp Glu
 330 335 340 345

AAA CCT GAA CCT TCT GAA CCT AGT AAA ACG TTT ATT GAT ACT TCA GTT Lys Pro Glu Pro Ser Glu Pro Ser Lys Thr Phe Ile Asp Thr Ser Val 350 355 360	1106
GCA AAG GAT GTT GAT AAT TCT ACA CAG GCG AAC CAT AAA AAG AAG AAA Ala Lys Asp Val Asp Asn Ser Thr Gln Ala Asn His Lys Lys Lys Lys 365 370 375	1154
AGT AAA TCT AAG CCG AGG AAA ACG GAA CCG GAA GAT GAA ATT GAA AAA Ser Lys Ser Lys Pro Arg Lys Thr Glu Pro Glu Asp Glu Ile Glu Lys 380 385 390	1202
GCT TTG AAA GAA ATT CAA GCT AGT GAG AAA AAA CTT ACG AAG TCT ATC Ala Leu Lys Glu Ile Gln Ala Ser Glu Lys Lys Lys Thr Lys Ser Ile 395 400 405	1250
GAT AAC ATT GTG AAT AAA TTT AAT ACA CCA CTT GCT AGT GTT AAA GCC Asp Asn Ile Val Asn Lys Phe Asn Thr Pro Leu Ala Ser Val Lys Ala 410 415 420 425	1298
GAT GAT TCC AAT TCT ACC AAG GAT AAT GTA CCA GCA AAG AAG AAA AAA Asp Asp Ser Asn Ser Thr Lys Asp Asn Val Pro Ala Lys Lys Lys Lys 430 435 440	1346
CCT TCG AAG TCA TCT GTT TCT TTA CCT GAG AAT GTA GTA CAA AAT CTA Pro Ser Lys Ser Ser Val Ser Leu Pro Glu Asn Val Val Gln Asn Leu 445 450 455	1394
TTG ATA CTA ACA TAA CTACTAGTAG CGACAAGATT GAAAACATGC CGCAACCGCA Leu Ile Leu Thr 460	1449
ACCAAAAAAGA GAAGATTTAC AAGATGCAGC TAAGGAAGTA TTGACTTCAA TAGAGTCAGT AATGATGCAG TCTGTTGAGA CTATTCCTAT TACGAAGAAA AGAGTAAATA AGAAAAAGAA TACCACTCAA CAGACGAAGG AATTTGTGGA ACACGAAATA TGCGATACAT CAAAAAAATGA AACTTTAAAAA AATATTGAAA AAGAATCGCA TGAGAATATG GCTATATTGC AAACAAGTCC GAAACCGCCA CTAAG	1509 1569 1629 1689 1704

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Pro Gln Ser Leu Ser Trp Gln Leu Pro Thr Gln Val Val Gln 1 5 10 15
Pro Val Phe Glu Gln Gln Met Gln Ile Pro Gly Tyr Asn Met Gln Ile 20 25 30
Gln Ser Asn Tyr Tyr Gln Ile His Pro Glu Met Leu Asp Pro Asn Leu

35	40	45
Asn Asn Pro Gln Gln Leu Met Phe Asn Tyr Met Gln Leu Gln Gln Leu		
50	55	60
Gln Glu Leu Gln His Leu Ser Gln Gln Pro Met His His Glu Phe		
65	70	75
Glu His His Ile Pro Ile Pro Gln Glu Ala Thr Ser Thr Asn Tyr Gly		
85	90	95
Pro Ser Gly Gln Tyr Ile Thr Ser Asp Ala Thr Ser Tyr Gln Ser Ile		
100	105	110
Ala Gln Gln Phe Val Pro Gln Pro Pro Ile Glu Thr Thr Thr Lys		
115	120	125
Ile Pro Glu Thr Glu Ile Gln Ile Gly Val Ser Asn Gln Tyr Ala Gln		
130	135	140
Asn Ile Thr Tyr Asn Ser Asn Ile Ser Pro Glu Val Ile Gly Phe Arg		
145	150	155
Glu His Tyr Val Ala Glu Gln Pro Ser Gly Asp Val Leu His Lys Ser		
165	170	175
His Leu Thr Glu Gln Pro Ala Asp Lys Ser Thr Arg Gly Asp Gln Glu		
180	185	190
Pro Val Ser Glu Thr Gly Ser Gly Phe Ser Tyr Ala Gln Ile Leu Ser		
195	200	205
Gln Gly Leu Lys Pro Thr Gln Pro Ser Asn Ser Val Asn Leu Leu Ala		
210	215	220
Asp Arg Ser Arg Ser Pro Leu Asp Thr Lys Thr Lys Glu Asn Tyr Lys		
225	230	235
Ser Pro Gly Arg Val Gln Asp Ile Thr Lys Ile Ile Asp Glu Lys Gln		
245	250	255
Lys Ser Ser Lys Asp Thr Glu Trp His Asn Lys Lys Val Lys Glu His		
260	265	270
Lys Lys Val Lys Asp Ile Lys Pro Asp Phe Glu Ser Ser Gln Arg Asn		
275	280	285
Lys Lys Ser Lys Asn Ile Pro Lys Gln Ile Glu Asn Ile Thr Pro Gln		
290	295	300
Leu Asp Ser Leu Arg Ser Arg Asp Ile Val Ile Lys Gly Glu Leu Leu		
305	310	315
Thr Lys Asp Thr Thr Lys Ser Leu Thr Thr Val Asn Val Asp Ser Glu		
325	330	335
Leu Asp Ser Val Lys Pro Lys Asp Glu Lys Pro Glu Pro Ser Glu Pro		
340	345	350
Ser Lys Thr Phe Ile Asp Thr Ser Val Ala Lys Asp Val Asp Asn Ser		
355	360	365

Thr Gln Ala Asn His Lys Lys Lys Ser Lys Ser Lys Pro Arg Lys
 370 375 380
 Thr Glu Pro Glu Asp Glu Ile Glu Lys Ala Leu Lys Glu Ile Gln Ala
 385 390 395 400
 Ser Glu Lys Lys Leu Thr Lys Ser Ile Asp Asn Ile Val Asn Lys Phe
 405 410 415
 Asn Thr Pro Leu Ala Ser Val Lys Ala Asp Asp Ser Asn Ser Thr Lys
 420 425 430
 Asp Asn Val Pro Ala Lys Lys Lys Pro Ser Lys Ser Ser Val Ser
 435 440 445
 Leu Pro Glu Asn Val Val Gln Asn Leu Leu Ile Leu Thr
 450 455 460

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGGAACCTC AATCGCTGTC TTGGCAACTT CCGACTCAAG TAGTTCAGCC AGTTTTTGAA	60
CAACAAATGC AGATTCTGG ATATAATATG CAAATTCAAT CTAATTATTA TCAAATTAC	120
CCAGAAATGT TGGATCCAAA TTTGAACAAT CCTCAGCAGT TAATGTTAA TTATATGCAA	180
TTACAACAAT TGCAGGAACt ACAACATTAA AGTCAACAAAC AGCCAATGCA TCATGAATT	240
GAACATCATA TCCCCATTCC ACAAGAAGCA ACTTCAACTA ATTACGGTCC ATCCGGACAG	300
TATATTACTA GTGACGCAAC ATCTTATCAA TCAATTGCC AACAAATTGT ACCACAACCA	360
CCAATTGAAA CTACCACAC GAAAATACCT GAAACTGAAA TTCAAATTGG CGTTTCGAAT	420
CAATATGCCC AAAATATAAC TTATAATTCA AATATCAGTC CTGAAGTGAT TGGATTCCGA	480
GAACATTATG TTGCGGAACA GCCTTCTGGT GACGTGCTTC ACAAAAGTCA TTTAACAGAA	540
CAACCAGCAG ATAAAAGCAC ACGTGGTGAT CAGGAACCTG TTAGTGAGAC AGGCTCTGGT	600
TTTCGTATG CACAAATTAA ATCACAGGGA CTTAACGCTA CCCAGCCATC CAACTCAGTT	660
AATTTGCTTG CAGATCGATC GAGATCACCT CTAGATACGA AAACGAAAGA AAATTATAAA	720
TCTCCTGGTC GTGTGCAGGA TATCACGAAA ATAATAGATG AGAAACAAAA GTCGTCAAA	780
GACACAGAGT GGCATAATAA GAAAGTGAAA GAACATAAAA AAGTGAAAGA TATCAAACCT	840
GATTTCGAAT CTTCTCAAAG GAATAAGAAA AGCAAGAATA TTCCTAAGCA AATTGAAAAT	900

ATCACACCTC AACTTGACAG CTTACGATCA CGAGATATAG TAATTAAGGG AGAATTACTA 960
 ACAAAAGATA CTACAAAAAG TTTAACTACT GTTAATGTTG ATAGTGAATT AGATAGTGT 1020
 AAACCTAAAG ATGAAAAACC TGAACCTTCT GAACCTAGTA AAACGTTAT TGATACTTCA 1080
 GTTGCAAAGG ATGTTGATAA TTCTACACAG GCGAACCAT AAAAGAAGAA AAGTAAATCT 1140
 AAGCCGAGGA AAACGGAACC GGAAGATGAA ATTGAAAAAG CTTTGAAAGA AATTCAAGCT 1200
 AGTGAGAAAA AACTTACGAA GTCTATCGAT AACATTGTGA ATAAATTAA TACACCACTT 1260
 GCTAGTGT AAGCCGATGA TTCCAATTCT ACCAAGGATA ATGTACCAGC AAAGAAGAAA 1320
 AAACCTTCGA AGTCATCTGT TTCTTACCT GAGAATGTAG TACAAAATCT ATTGATACTA 1380
 ACA 1383

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1758 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1...1758

(ix) FEATURE:
 (A) NAME/KEY: W = A or T
 (B) LOCATION: 1136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTA GAG ATG GCT AAA TTT CTG ACG GAA ACA TTA GAC GAC ATG ACT CTA 48
 Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu
 1 5 10 15

CAA CAC AAA GAT CAC AGA TCA GAA TTG GCT AAA GAG TTT TCA ATT TGG 96
 Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp
 20 25 30

TTT ACG AAA ATG AGA CAG TCT GGC GCT CAA GCC AGT AAC GAA GAA ATC 144
 Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile
 35 40 45

ATG AAA TTT TCA AAA TTG TTT GAA GAT GAA ATC ACT CTT GAC TCG CTG 192
 Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu
 50 55 60

GCG AGG CCG CAA CTT GTT GCT TTG TGC AGG GTA CTA GAA ATC AGT ACT 240
 Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr
 65 70 75 80

TTA GGA ACA ACA AAT TTC TTA AGG TTT CAA CTG CGA ATG AAA CTG CGT 288
 Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg
 85 90 95

TCA TTA GCT GCT GAT GAT AAA ATG ATT CAA AAA GAA GGC ATA GTT TCT 336
 Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser
 100 105 110

ATG ACT TAT TCG GAG GTG CAA CAG GCC TGC AGA GCT CGT GGA ATG CGA 384
 Met Thr Tyr Ser Glu Val Gln Ala Cys Arg Ala Arg Gly Met Arg
 115 120 125

GCT TAT GGT ATG CCT GAA CAT AGG TTG AGG AGG CAA TTG GAA GAC TGG 432
 Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp
 130 135 140

ATT AAT TTA AGC TTG AAT GAA AAG GTT CCA CCA TCA TTA TTG CTT TTG 480
 Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu
 145 150 155 160

TCA AGG GCG CTG ATG TTG CCC GAG AAT GTT CCA GTG TCT GAT AAA CTT 528
 Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu
 165 170 175

AAA GCA ACA ATA AAT GCT CTT CCT GAA ACT ATT GTA ACT CAG ACA AAG 576
 Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys
 180 185 190

GCT GCT ATT GGA GAA AGA GAA GGA AAG ATT GAC AAT AAG ACC AAA ATT 624
 Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile
 195 200 205

GAG GTC ATC AAA GAG GAA GAA CGC AAA ATT CGC GAA GAG CGC CAA GAA 672
 Glu Val Ile Lys Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu
 210 215 220

GCA CGT GAG GAA GAG GAA CAA CGC AAG CAA GCC GAA CTT GCT CTT AAT 720
 Ala Arg Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn
 225 230 235 240

GCC AGT TCT GCA GCA GCT GAG GCC TCT TCA GCT CAG GAA CTT TTG ATA 768
 Ala Ser Ser Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile
 245 250 255

GAT ACA GCT CCT GTA ATA GAT GCA GAA AAG ACA CCA AAG GTG GCA ACA 816
 Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr
 260 265 270

TCA CCT GTT GAA TCA CCA TTG GCA CCA CCA GAA GTT CTG ATT ATG GGT 864
 Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly
 275 280 285

GCT CCT AAA ACA CCT GTT GCA ACC GAA GTG GAT AAG AAT GCT GAT GAG 912
 Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu
 290 295 300

GTG GAA TTC ACC AAG AAA GAT CTT GAG GTT GTT GAA GAT GCA TTG GAT 960
 Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp
 305 310 315 320

ACA CTA TCG AAA GAC AAA AAT AAT TTG GTG ATT GAA AAG GAA GTT ATT 1008
 Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile
 325 330 335

AAA GAC ATT AAG GAA ATT GCT GAT TAC CAA GAA GAT GTA GAA GAA Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu 340 345 350	1056
TTG AAA GAA GCC ATA GTT GCT GAG AAA CCA AAG GAT GAG ATA AAA Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys 355 360 365	1104
GAA ACT AAA GGA GCT CAA CGA TTG TTG AAG AWG GTT AAC AAG ATG ATA Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile 370 375 380	1152
ACG AAA ATG GAT ACT GTT GTA CAA GAA ATT GAA AGC AAA GAA TCT GAG Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu 385 390 395 400	1200
AAG AAA GCC AAA ACA TTG CCA CTT GAA GCT CCT AGG AGC GCT ACT GAA Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu 405 410 415	1248
ACT CAA GAA TTA GAT GTA AGG AAA GAA AGA GGA GAG ATT TTA ATT GAC Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp 420 425 430	1296
GAA TTA ATG GAC GCT ATT AAG AAA GTT AAA AAT GTG CCA GAC GAA AAT Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn 435 440 445	1344
CGC TTG AAA TTA ATT GAG AAC ATT TTG GGC AGG ATC GAT ACT GAC AAA Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys 450 455 460	1392
GAT AGG CAT ATC AAA GTT GAA GAT GTA TTG AAG GTT ATT GAC ATT GTG Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val 465 470 475 480	1440
GAA AAA GAA GAT GGT ATC ATG AGT ACA AAA CAA TTA GAT GAG TTG GTT Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val 485 490 495	1488
CAG CTT TTG AAA AAG GAG GAA GTT ATT GAA TTG GAA GAA AAG AAA GAA Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu 500 505 510	1536
AAG CAA GAG TCT CAA CAG AAA AGT TTT GTA CCA CCA AGT GAA ACT TTG Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu 515 520 525	1584
CAT CTT GAA TCA TCA CAG CAG AAG AGT ACA GTT CCT AGC TCG GGA CAT His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His 530 535 540	1632
GAA GCT AAG GTG TCC GAA GAT GAC TTA AAT GTT AAA AAT AAA AAT TTG Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu 545 550 555 560	1680
GAA GAA TCG ACC AAA ACT GAA TGT GGA GCA ATT GAC GAA GAG CAC AGA Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg 565 570 575	1728
AGA GAG CAT TGC CAG TAC CCA GAC ATT ACA	1758

Arg Glu His Cys Gln Tyr Pro Asp Ile Thr
580 585

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 586 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Xaa = any amino acid
(B) LOCATION: 379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu
1 5 10 15

Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp
20 25 30

Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile
35 40 45

Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu
50 55 60

Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr
65 70 75 80

Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg
85 90 95

Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser
100 105 110

Met Thr Tyr Ser Glu Val Gln Gln Ala Cys Arg Ala Arg Gly Met Arg
115 120 125

Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp
130 135 140

Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu
145 150 155 160

Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu
165 170 175

Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys
180 185 190

Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile
195 200 205

Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu
210 215 220

Ala Arg Glu Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn
 225 230 235 240
 Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile
 245 250 255
 Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr
 260 265 270
 Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly
 275 280 285
 Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu
 290 295 300
 Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp
 305 310 315 320
 Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile
 325 330 335
 Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu
 340 345 350
 Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys
 355 360 365
 Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile
 370 375 380
 Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu
 385 390 395 400
 Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu
 405 410 415
 Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp
 420 425 430
 Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn
 435 440 445
 Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys
 450 455 460
 Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val
 465 470 475 480
 Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val
 485 490 495
 Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu
 500 505 510
 Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu
 515 520 525
 His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His
 530 535 540
 Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu

545 550 555 560

Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg
565 570 575

Arg Glu His Cys Gln Tyr Pro Asp Ile Thr
580 585

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCCGGGCTGC AGGAATTCGG CACGAGATGA GAATGGAAAT GTGATTAGCT ATACTGATGA 60
AAATGGAAAC ATTATCAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA TTACTGATGA 120
AAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAC ATTATCAGTA CTACTGATGA 180
GAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAT GTGATTAGCA TTACTGATGA 240
AAATGGAAAC ATTATTAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA ATA 293

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTGGAAACAG CTATGACCAT GATTACCCA AGCTCGAAAG TTAAVCCCTC ACTHARAGGG 60
GAACAAAAGT CTGGAGCTCC ACCCGCGGAT GGCGGCCGCB TCTAGAACCT AGTGGACTCC 120
CCCGGSGCTG CAGGAATTCTG GGCACGAGCT CCAGCTAGCC ATATAACATTC ATCCAAAATG 180
AAGTTGSAAT GTGTCTTACCGGCAACGGG ATGCCAGAAA TTGTGKTCGAA ATKTGTGGAC 240
GAGCACAAAGC TTCGTGTCTK TCTATGAAAA ACGTATGGGA GCAGAAAGTCG AGGGCCGACA 300
TCCTCGCGA TGAATGGARA GGTTATGTGC TCCGA 335

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATAGCTTTA ATATTTTAA TTGATGTATT GCTCAATGGT GATTTCTGTT TATTAACGT	60
AGTTACCAAT ATGCTCGCTT CAATAGACAT AGCAAATGAA AGCATTCCGT ATCCTCAAGC	120
GTTACCAAAAC TAACATTAAG GAGTTAAATA AATGTTGTTT CCAATAAATA TAATGGGAAA	180
AACATTTAAT ATTTGTTCCA ATTTGTATTT ATTTTTACTA CAATTATATA CAATAAAATA	240
TTTTTATATA TATTTTATAA AGTTTATGAT GCAGGAGAGA AAATAATGTT AAGAATATAG	300
GTAATGTGTA TATATAAAATG TTTGACAAGC ATGTTCTAGT TAAATAATAA ATACAATGTT	360
AAATCTACTT AAAAAAAAAA AAAAAAAAAA AAAAAAA	396

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGAAAGCGAA GAATGAAAAG GGGAAACAAA AAAAGAAAAG ACGAAGGAGT GGAGAGATAA 60
AACGGAGGCA AAGAAAGAAAA TGAGGATGCA AAAGAAAAGGT AATAAAAGAG ATGAAAAGAA 120
GGAAAAAGGA AATAACAAAG AAAGAGTGAG GGAAAAATAA AGACAGAGGC GAAGCAAAAA 180
AGGAGGAGAA ATAGAGATTA AAAAAGAAAT ACAGCGAAGA AACCCAGGAAA GCGATAAAAGA 240
AAAAAAAAAGA AAAAAAGAGA GCAGTGAAGA AAAAAAAAAAA AAAAAA 285

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAGATATTTCCTAAAYATTGTGAAAYAAATCATTTCAGGTSTCCAAAGTGTTCGCTCTTGCCATCAATGGCTTTATAGGGGGCTSCACAAGYCTTTTTTCGACAAAGATGMC
GTCTTAGATAASATSGTAGA TRACATCTCTGRCTSMATATGAGAACARCA TTGSMAGAAT
TAGCCAAGGRTNGCRAAATTGATATGMTTS CYGCTGTAATTTCGAAAAA 60
120
180
228

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTT CGT GTC AAC CGC TGG GTC AGA CCT GTT ATT GCT ATG CAC CCA ACC	48
Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr	
1 5 10 15	
ATG ACT CTT GCT GAA CGT CTC GGC AAA AAA GCT TTG CGC GAC CAA TAT	96
Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr	
20 25 30	
GCT CCC GTT TGC TCC ATT GGA CAA CGT AAC ATC AAC ACC TTT GAC AAC	144
Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn	
35 40 45	
ATG ACC TTC CCC GCT CAA TTC GGA AAA TGC TGG CAC GCT TTG TTG CAA	192
Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln	
50 55 60	
ACT GTT CCC CAA AAG TAT TCC GAA GAA CGT GAA TAC AGC GAA GAA CAA	240
Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln	
65 70 75 80	
CAA TAC GAC CGT CAA ATG TCC GTC CTC GTT CGT GAA AAC GGC GAA GAA	288
Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu	
85 90 95	
AAA AGA CGT TAT GAT TGT CTT GGG CAA CCG TTA CAA CAA TTG AAT TGC	336
Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys	
100 105 110	
AAT	339
Asn	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr	
1 5 10 15	

Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr
 20 25 30

Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn
 35 40 45

Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln
 50 55 60

Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln
 65 70 75 80

Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu
 85 90 95

Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys
 100 105 110

Asn

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCC AGC TCC TCC AGC TCC AGC AGT GAC TCT TCC AGC TCC AGC AGC TCT	48
Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser Ser Ser	
1 5 10 15	
TCC TCT TCC AGC TCC AGC TCC TCT TCT GAA TCT TCC GAA GAA AAA	96
Ser Glu Ser Ser Glu Glu Lys	
20 25 30	
ACC TCC CAC AAA AAA TCC GAA AAG AAG GAA CAC AAA TCC TGC TCC ATC	144
Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile	
35 40 45	
AAG AAG CAA GTA CAA TTC GTA GAA AAA GAC GGT AAA CTC TGC TTC AGC	192
Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser	
50 55 60	
ATC CGT CCC TTG GCC GCT TGC CAA AAA CAC TGC AAA GCC ACT GAA ACC	240
Ile Arg Pro Leu Ala Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr	
65 70 75 80	
ACT CAA ATG GAA GTC GAA GTA TAC TGC CCC TCT GGC AGC CTT GCT GAA	288
Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu	
85 90 95	

CTT TAC AAA CAA AAG ATC CTT AAG GGA GCC AAC CCC GAC TTG AGC GAC 336
Leu Tyr Lys Gln Lys Ile Leu Lys Gly Ala Asn Pro Asp Leu Ser Asp
100 105 110

AAG ACT CCT TCC AGA ATC TTG AAA TTC AAG GTT CCC AAA GCT TGC ACC 384
Lys Thr Pro Ser Arg Ile Leu Lys Phe Lys Val Pro Lys Ala Cys Thr
115 120 125

GCT TAC TAAATCTGAA ATAAATTACA TGGATTAGTT CATTCTGAT GTAGTGCAAT 440
Ala Tyr
130

TAGTCGATA ATAAATTATT CAATGAGCAT TTAAAAAAA AAAAAAAA AAC 493

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser
1 5 10 15

Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Ser Glu Glu Lys
20 25 30

Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile
35 40 45

Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser
50 55 60

Ile Arg Pro Leu Ala Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr
65 70 75 80

Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu
85 90 95

Leu Tyr Lys Gln Lys Ile Leu Lys Gly Ala Asn Pro Asp Leu Ser Asp
100 105 110

Lys Thr Pro Ser Arg Ile Leu Lys Phe Lys Val Pro Lys Ala Cys Thr
115 120 125

Ala Tyr
130

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTAGTGCCAT CATTCTGAAA CTTTGTGACG GTCGGCGCT GTATWGGTGC TGCCTGGAAA	60
TTGCATCGAT GCACTWCCGT GTCGGCGCA WATAGTGCCK TGGSCCCTGT CTGTTATAG	120
ACATTCAAGG CGCGGSAKT AGCCATGTT ATGGCTCMCA AWMTGCATTC ACAGTGGGGT	180
CACATTCAG TCGCATGATT KMTCAARTTA GTATMWGADA TATATTTTA TCATACTAAG	240
TAGTGAGCDA ATAACACGCG ARWWACRAAC ACCGAATATC TTKAGTTTT GCACAGATAT	300
KTGTAA	306

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCGGATACG TTGCCAATGA CTACGTCACTT ACCAATGTTG TTTCCACTCC AGTTACTGGA	60
TACACCACCG GACATCTTGC TAATGACTAC GTCACCCACCA ATGTTGTATC CACTCCAGTT	120
ACTGGATACA CCACCGGACA TCTTGCAAT GACTACGTCA CCACCAACGT AGTTCCGCA	180
CCAGTCACCA CTGGATACAC CACTGGCTAT ACCACCGGTA ATGTCGGATA CACCACCGGA	240
GTTACTGGTT ACACCAACGG AGTTAGTGG A TATACCAATG GACTTAATGG TTATACCACT	300
GGTAGCTATG TCAGCTCCCC AGGATACACT TCTTCTGGAC TTGTCAACGT TTTCTAGATT	360
TATGATTTCG TCTGCCCTCA ATGATGATGA CCACACTTT TACTTTTAT GATATTTGGA	420
AAAAATAAAT AACTGGAAAGA ATATATAATA ATTTCAAAAT AAAAAAAA AAAAAAAA	480
CTCGAGGGGG	490

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAAAAATCGA AAGAAGGCCTT AAAACCAAAA TGGGCACAGA AGGATATTG GGATTTAGT	60
GATGCCGACA TGGAGAGGTT ACTGGATCAA TGGGAAGAAG ATGAAGACCC CCTTCCAGAA	120

GACGAATTGC CCGAACATCT CAGACCTGAT CCAAAGATCG ACATAAGCAA CATCGATATG	180
AGCAATCCCB AAAACATACT AAAGGCTTCC AAAAAAGGCA AGACTTGAT GGCATTGTA	240
CAAGTCAGTG GAAATCCAAC ACAAGAAGAA GCCGAAACCA TCACTAAATT GTGGCAAGGC	300
AGTCTATGGA ATAGTCATAT ACAAGCCGAA AGATATATGG TTAGCGATGA CAGGGCTATA	360
TTTATGTTTA AAGATGGTTC TCAAGCTTGG CCTGCTAAAG ACTTTTAGT GGAACAAGAA	420
AGGTGTAAAG ATGTTACAAT TGAAAATAAA ATATATCCTG GTAAATATTTC TTGACTAAA	480
GAAGAATTAT AATATAATAT ATTATAATTA TAATCTATAA AATAGATTTG AAATTCTACA	540
TTCATGATCT ACTATGTATG ATATTAATT ATTAAAAATA ATGTTTTTC AAGTAAAAAA	600
AAAAAAAAAAA AAAAAAA	616

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCGTGCAGG ACAGATATAG GACCGGATTG GTTAATTGAT TTGAGTGAAG TGGCTTCTGG	60
TGGTTCTGAT ATTGACACAA AATTTTCCAA TTTAAAAATA GATAAAAAGC CTGTTGCAAC	120
TTCACAAACAA GGAATTGATG AATTGATAT GTTTGCACAA TCGAGAAACA TTTCTAGTGA	180
GGGATCAACC AGTGCTATGA AGGAAGGACA CGGTTGGAC TTATTATCAA ATACACATAA	240
AAATGTACCA CCAACAATTC CACAAGCCGG ACAACTTCCA AGGGATTCTG AGTTTGATGA	300
AATTGCTGCT TGGCTTGATG AAAAGGTTGA AGACAAAGCC CAAGTTCCCG AAGACAGTAT	360
TACAAGCAGT GAATTTGATA AATTCTGGC AGAACGGCA GCTGTTGCTG AAACTTGCC	420
AAATATTCCA CCGACTACAC AAAGTAATCA TTCAAATATT GAAGCAAACG ATAAA	475

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCGGCACGGG AGGTAGTGAC GAAAAATAAC GATACGGGAC TCATCCGAGG CCCCCTAATC	60
GGAATGAGTA CACTTAAAT CCTTTAACGA GGATCTATTA GAGGGCCAGT CTGTGTGCCA	120

GCAGCCGCGG TAATTCCAGC TCTAATAGCG TATATTAAG TTGTTGCGGT TAAAAAGCTC	180
GTAGTTGAAT CTGTGTCCCA CACTGTYGGT TCACCGCTCG CGGTGTTCAA CTGGCATGTC	240
TGTGGGACGT CCTACCGGTG GGCTTAGCCC GTCAAAAGGC GGCCCAACTC AAAAT	295

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTGACTAATC CCAGGACTCC TTTATCCTGT TTGCGCAATG TCGATAACCA TCTCACAATG	60
GTAAATGATT TATCGGCTAA ACAGAAGAGT CCTAAGAAGG TTGTTAAAGG TGGTTCTAGA	120
ATACCGACTT TTAGACCCAA GGCTATGAAT GCTGATGTT AGAATTTGA TTCGATGAGG	180
TGCGATGTTT GGRACAAAGA CACCAAGTGT GTTATATAAT TACTAAAGCA ATCCACATGT	240
AGCTAATTTT TTTTTTACAA TTTTATTTGT AACTATGTGT ATTTATATGA ATTCTTGTGG	300
AATATAATTAA TAAGTTTTA AATGAAATAT AGATATTATT CTAAAAAAA AAAACAAAAA	360
AAAAAAAAAA AA	372

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGATTCCGCA CGAGAATTAA TTAAGCGCAT TATTTGCAAG TGTAATTGTC TCCTTTAACG	60
CGGAAGTACA AAATCGAACATC GTTGGTGGCA ATGATGTAAG TATTCAAAA ATTGGGTGGC	120
AAGTATCTAT TCAAAGTAAT AACCAACATT TCTGTGGTGG TTCAATCATT GCTAAAGATT	180
GGGTACTGAC TTCTTCTCAA TGCCTCGTGG ACAAACAAAG TCCACCGAAG GATTAACTG	240
TTCGTGTTGG AA	252

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTCCTGCTG TTAATAGTAC TAATGCAGTA ATTGCTGCHA GCTGCTGCAC AGAGGTTTT	60
AAAATGGCAA CAAGTTGTTA CACCCACATG AACAACTACA TGGTATTCAA TGATACCGAT	120
GGGATTTATA CATATACTTA CGAAGCTGAA AGAAAACCTG ACTGTTAGC TTGTTCACAA	180
ATTCCAAAAAA CTATAGAAGT TTCTAATCCT GAAAATATGA CTCTCCAAGA CTTGATTACT	240
TTGTTGTGTG AAGGGGCTGA ATATCAAATG AAGAGCCAG GTATTGTAGC CTCAATCGAA	300
GGCAAAAACA AAACCTTATA CATGTCAACA GTAGCAAGTA TAGAAGAAAA GACTAAACAG	360
AATCTAACAA AGTCTCTAAA AGAATTAAAT CTAGAAAATG GAATGGAACG GATGGTTGCA	420
GATGTGACGA CACCAAACAC AATATTACTT AAATTAAAAT ATAAGAATGT AATTGAAAAC	480
GATGTTGAGA TGACTTGATA TTTACTTAAA AATGTTATCT TACAATAATT GATAATTAT	540
ATTTAATACT TTTGGAACCTT TGTATTTAAT GATAATAAT TATTATAAGA ATTAAAAAAA	600
AAAAAAAAAAA AAA	613

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TT GAT ATT TGC TCT GTT GAG GGT GCC TTA GGA TTT TTA GTG GAA ATG	47
Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met	
1 5 10 15	
TTA AAA TAT AAG GCC CCA AGT AAA ACT CTA GCT ATT GTC GAG AAT GCT	95
Leu Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala	
20 25 30	
GGT GGA ATA TTA CGA AAT GTC TCT AGT CAT ATA GCC CTT AGA GAG GAC	143
Gly Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp	
35 40 45	
TAC AGA GAA ATA CTT CGA CAT CAT AAT GTC TTA ACA ATA TTA CTA CAA	191
Tyr Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln	
50 55 60	
CAA TTA AAA TCA CCA AGC CTC ATA ATT GTC AGT AAT GCT TGT GGG ACA	239

Gln Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr			
65	70	75	
TTA TGG AAT TTA TCT GCT AGG AAT TCA ACA GAT CAA CAA TTT TTA TGG			287
Leu Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp			
80	85	90	95
GAG AAT GGT GCT GTC CCT TTA TTA AGA AGT TTG ATA TAT TCT AAG CAT			335
Glu Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His			
100	105	110	
AAA ATG ATA TCT ATG GGA TCA AGT GCA GCT CTC AAA AAT TTG TTA AAT			383
Lys Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn			
115	120	125	
GCA AAA CCT GAG TGC ATC AAT TTC TTA AGT GAT TCT TCT AAA GGA			431
Ala Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Lys Gly			
130	135	140	
GTT CCA AAT CTA ACT ACA TTG GGT GTA AGA AAA CAA AAA TCT CTA CAT			479
Val Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His			
145	150	155	
GAG TTA ATA GAT CAA AAT CTT TCA GAA ACT TGT GAT AAT ATA GAT AGT			527
Glu Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser			
160	165	170	175
GTG GCC GCT AA			538
Val Ala Ala			

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met Leu			
1	5	10	15
Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala Gly			
20	25	30	
Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp Tyr			
35	40	45	
Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln Gln			
50	55	60	
Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr Leu			
65	70	75	80
Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp Glu			
85	90	95	
Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His Lys			

100 105 110

Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn Ala
 115 120 125

Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Ser Lys Gly Val
 130 135 140

Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His Glu
 145 150 155 160

Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser Val
 165 170 175

Ala Ala

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTT CTT CTT AAA CAG TTG GAC TCT GGA TTG TTA CTT GTT ACA GGT CCC	48
Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Val Thr Gly Pro	
1 5 10 15	
TTC TTA ATC AAT GCA TGC CCA TTG CGT CGC ATT TCC CAA AAC TAT GTC	96
Phe Leu Ile Asn Ala Cys Pro Leu Arg Arg Ile Ser Gln Asn Tyr Val	
20 25 30	
ATT GCC ACC TCT ACC CGA TTA GAC GTT AGT GGA GTT AAA TTA CCA GAA	144
Ile Ala Thr Ser Thr Arg Leu Asp Val Ser Gly Val Lys Leu Pro Glu	
35 40 45	
CAC ATC AAT GAT GAT TAT TTC AAA AGG CAA AAG AAC AAG CGT GCA AAG	192
His Ile Asn Asp Asp Tyr Phe Lys Arg Gln Lys Asn Lys Arg Ala Lys	
50 55 60	
AAA GAG GAA GGT GAT ATT TTT GCT GCC AAG AAA GAG GCT TAT AAA CCA	240
Lys Glu Glu Gly Asp Ile Phe Ala Ala Lys Lys Glu Ala Tyr Lys Pro	
65 70 75 80	
ACT GAG CAA AGG AAG AAT GAC CAA AAG CTT GTA GAC AAA ATG GTT TTA	288
Thr Glu Gln Arg Lys Asn Asp Gln Lys Leu Val Asp Lys Met Val Leu	
85 90 95	
GGA GTA ATC AAG AAG CAC CCA GAC CAC AAA CTT TTG TAT ACA TAT TTG	336
Gly Val Ile Lys Lys His Pro Asp His Lys Leu Leu Tyr Thr Tyr Leu	
100 105 110	

TCA GCT ATG TTT GGT TTG AAA TCT TCC CAA TAT CCA CAT CGT ATG AAG 384
Ser Ala Met Phe Gly Leu Lys Ser Ser Gln Tyr Pro His Arg Met Lys
115 120 125

TTC T AAATACTATA TTCATAAAAT AAATTGAAC TCTCAAAAAA AAAA 432
Phe

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly Pro
1 5 10 15

Phe Leu Ile Asn Ala Cys Pro Leu Arg Arg Ile Ser Gln Asn Tyr Val
20 25 30

Ile Ala Thr Ser Thr Arg Leu Asp Val Ser Gly Val Lys Leu Pro Glu
35 40 45

His Ile Asn Asp Asp Tyr Phe Lys Arg Gln Lys Asn Lys Arg Ala Lys
50 55 60

Lys Glu Glu Gly Asp Ile Phe Ala Ala Lys Lys Glu Ala Tyr Lys Pro
65 70 75 80

Thr Glu Gln Arg Lys Asn Asp Gln Lys Leu Val Asp Lys Met Val Leu
85 90 95

Gly Val Ile Lys Lys His Pro Asp His Lys Leu Leu Tyr Thr Tyr Leu
100 105 110

Ser Ala Met Phe Gly Leu Lys Ser Ser Gln Tyr Pro His Arg Met Lys
115 120 125

Phe

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 47..313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

10031354020202

TGGAAATTCA ATATTTGTT TTAACATTAATTTTCAAA TTGAT ATG AAA TTT	55
Met Lys Phe	
1	
TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA GAA TCT ATG	103
Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln Val Ser Met	
5 10 15	
TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT AAT CCA AGT	151
Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser	
20 25 30 35	
ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT	199
Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe	
40 45 50	
TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA AGT CAA TGT	247
Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys	
55 60 65	
GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT	295
Gly Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr Arg Pro Asn	
70 75 80	
CAA AAA CAC TGT TAT TGC GA ATAACCATAT TCCGGATGAA AGACCAAATT	345
Gln Lys His Cys Tyr Cys	
85	
GATATAAATT ACTAAAATTA TGCTAGATAG CAATCATAAA ATTTGAAAGT TTTCAATGAT	405
CCTAACATGT TTTGCCTCCA ATTTATTTA ACAGCAAATT GCTGGGAAC TACCGTACCG	465
TAACAAAATG TTCAAGAAAT ACTGAATGTT TACAAATAGA TTATTATAAA TATTGTAACA	525
TTGTCTAATA TTTATAAGAA TTATATAAAC TGAATTGCAA AAGTTGAAAA AAAAAAAA	585
AAAAAAA	595

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln	
1 5 10 15	
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn	
20 25 30	
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile	
35 40 45	
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys	
50 55 60	

Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr
65 70 75 80

Arg Pro Asn Gln Lys His Cys Tyr Cys
85

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTTTTTTTT TTTTTTTTT TTTTCAACTT TTGCAATTCA GTTTATATAA TTCTTATAAA	60
TATTAGACAA TGTTACAATA TTTATAATAA TCTATTTGTA AACATTCAGT ATTTCTTGAA	120
CATTTGTTA CGGTACGGTA AGTTCCCAGC AATTTGCTGT TAAAATAAT TGGAGGCAA	180
ACATGTTAGG ATCATTGAAA ACTTCAAAAT TTTATGATTG CTATCTAGCA TAATTTTAGT	240
AATTTATATC AATTTGGTCT TTCATCCGGA ATATGGTTAT TCGCAATAAC AGTGTTCG	300
ATTTGGTCGT GTTGAACCAC CGTTCCACA AGCACCACCT CCAAATCCAC ATTGACTTT	360
GCAAAATATT TTGCAACTT GATGATTCC AATACAAAAA TCTTCAATAG TAAGCTTCCC	420
AGATGGTATT GACACCTCTT TTGTACTTGG ATTATTCCT CCCGATTTAC ACTTTTCAGT	480
GACCATTTT GACATAGATA CTTGATTAA TAAAACACAC AACACGCAA TTGCCAGTAA	540
AAATTCATA TCGAATTGA AAAATTAAAT GTTAAACAA AATATTGAAT TTCCA	595

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA	48
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln	
1 5 10 15	
GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT	96
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn	

20	25	30	
AAT CCA AGT ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT			144
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile			
35	40	45	
GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA			192
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys			
50	55	60	
AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA			240
Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr			
65	70	75	80
CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA			270
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu			
85	90		

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln			
1	5	10	15
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn			
20	25	30	
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile			
35	40	45	
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys			
50	55	60	
Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr			
65	70	75	80
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu			
85	90		

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTCGCAATAA CAGTGTGTTT GATTGGTCG TGTTGAACCA CCGTTCCAC AAGCACCACC

60

TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA	120
ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTCC	180
TCCCGATTAA CACTTTCAAG TGACCATTAA TGACATAGAT ACTTGATTAA ATAAAACACA	240
CAACACGCAA ATTGCCAGTA AAAATTCAT	270

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT AAT CCA AGT	48
Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser	
1 5 10 15	

ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT	96
Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe	
20 25 30	

TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA AGT CAA TGT	144
Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys	
35 40 45	

GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT	192
Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn	
50 55 60	

CAA AAA CAC TGT TAT TGC GAA	213
Gln Lys His Cys Tyr Cys Glu	
65 70	

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser	
1 5 10 15	

Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe	
20 25 30	

Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
35 40 45

Gly Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr Arg Pro Asn
50 55 60

Gln Lys His Cys Tyr Cys Glu
65 70

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TTCGCAATAA CAGTGTAAAA GATTTGGTCG TGTTGAACCA CCGTTTCCAC AAGCACCACC 60
TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA 120
ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC 180
TCCCGATTAA CACTTTTCAG TGACCATTAA TGA 213

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGG AAA GTT AAT AAA AAA TGT ACA TCA GGT GGA AAA AAT CAA GAT AGA 48
Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg
1 5 10 15
AAA CTC GAT CAA ATA ATT CAA AAA GGC CAA CAA GTT AAA ATC CAA AAT 96
Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn
20 25 30
ATT TGC AAA TTA ATA CGA GAT AAA CCA CAT ACA AAT CAA GAG AAA GAA 144
Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu
35 40 45
AAA TGT ATG AAA TTT TGC AAA AAA GTT TGC AAA GGT TAT AGA GGA GCT 192
Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala
50 55 60

TGT GAT GGC AAT ATT TGC TAC TGC AGC AGG CCA AGT AAT TTA GGT CCT Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro 65 70 75 80	240
GAT TGG AAA GTA AGC AAA GAA TGC AAA GAT CCC AAT AAC AAA GAT TCT Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser 85 90 95	288
CGT CCT ACG GAA ATA GTT CCA TAT CGA CAA CAA TTA GCA ATT CCA AAT Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Ile Pro Asn 100 105 110	336
ATT TGC AAA CTA AAA AAT TCA GAG ACC AAT GAA GAT TCC AAA TGC AAA Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys 115 120 125	384
AAA CAT TGC AAA GAA AAA TGT CGT GGT GGA AAT GAT GCT GGA TGT GAT Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp 130 135 140	432
GGA AAC TTT TGT TAT TGT CGA CCA AAA AAT AAA TAATAATTAT AATAAATAAA Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys 145 150 155	485
TTGTTATAGT TATTAGTTAT CCCATCACAT ATTAGAAAAG TGGCTTATAA TTTATGAACA	545
ATATAACACA TAAATTAGTT GTGTAATTTC GAATGTTTTT TTCAAATATA AGGCGTTTT	605
CTAGAATATC TTGATATTAG AAACTAACCT AGATTATTTT GTTGTGTATA AAATATTCAA	665
ATACGTAAGT TATATTGAAC AAAGCATTAA GAAGCTACAT TAGATATACT AAATAAGTGC	725
AAAATTGCAT GGAAACCCCTT ACTGGATTAA CTACATATTT TCTTCCTAAA TATTGTCTTG	785
GTATTACTCT TATTATATAA AAATTAATAT AAAATTGTAG ACAGAGACGA ATTGGGGTAT	845
TGTTATATAT AAAAAAGTAG TGGATTATTT AATTCTAAAA AAGTTTGCAA AATGTTTCAT	905
ACATAATAAC CGAATATTAA CAAATATATA AATATTGTAA TGAATAATG CGCATCTGTA	965
TGCTTAATAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	1007

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg
1 5 10 15

Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn
20 25 30

Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu

35	40	45
Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala		
50	55	60
Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro		
65	70	75
Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser		
85	90	95
Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Ile Pro Asn		
100	105	110
Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys		
115	120	125
Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp		
130	135	140
Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys		
145	150	155

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTT TTATATTAAG CATAACAGATG CGCATTATTATT	60
CATTACAATA TTTATATATT TGAAAATATT CGGTTATTAT GTATGAAACA TTTTGCAAAC	120
TTTTTTAGAA TTAAATAATC CACTACTTT TTATATATAA CAATACCCCA ATTCTGTCTCT	180
GTCTACAATT TTATATTAAT TTTATATATAA TAAGAGTAAT ACCAAGACAA TATTTAGGAA	240
GAAAATATGT AGTAAATCCA GTAAGGGTTT CCATGCAATT TTGCACATTAT TTAGTATATC	300
TAATGTAGCT TCTAAATGCT TTGTTCAATA TAACTTACGT ATTTGAATAT TTTATACACA	360
ACAAAATAAT CTAAGTTAGT TTCTAATATC AAGATATTCT AGAAAAACGC CTTATATTTG	420
AAAAAAACAT TCGAAATTAC ACAACTAATT TATGTGTTAT ATTGTTCAATA AATTATAAGC	480
CACTTTCTA ATATGTGATG GGATAACTAA TAACTATAAC AATTATTTA TTATAATTAT	540
TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCCATCAC ATCCAGCATC ATTTCCACCA	600
CGACATTTTT CTTTGCATG TTTTTGCAT TTGGAATCTT CATTGGTCTC TGAATTTTT	660
AGTTTGCAAA TATTTGGAAT TGCTAATTGT TGTCGATATG GAACTATTTC CGTAGGACGA	720
GAATCTTGT TATTGGATC TTTGCATTCT TTGCTTACTT TCCAATCAGG ACCTAAATTA	780

CTTGGCCTGC TGCAGTAGCA AATATTGCCA TCACAAGCTC CTCTATAACC TTTGCAA	840
TTTTGCAAA ATTCATACA TTTTCTTTC TCTTGATTTG TATGTGGTTT ATCTCGTATT	900
AATTGCAAA TATTTGGAT TTTAACTTGT TGGCCTTTT GAATTATTTG ATCGAGTTT	960
CTATCTTGAT TTTTCCACC TGATGTACAT TTTTATTAA CTTTCCA	1007

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCA GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA	48
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr	
1 5 10 15	
CCT TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT	96
Pro Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp	
20 25 30	
TCA AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC	144
Ser Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly	
35 40 45	
AAA TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG	192
Lys Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp	
50 55 60	
GAT TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT ACG AGA AGA TCT	240
Asp Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser	
65 70 75	
CAA GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA GAA AAG GAA AAG	283
Gln Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys	
80 85 90 95	
GCA GTT TGG ACA AAA GAG AAA GGA GAT AAA ACC ATA TTT TCT TCG TTT	336
Ala Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe	
100 105 110	
GGT GAA TAT GCT AAA TTT TAT AGT CCA AAA ACT TGT CCA AAC TTC ATA	384
Gly Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile	
115 120 125	
GCA CAA CAG AAA ATA GCA GTA AGA GAC TTG TTA ACA AAA AGT GCA AAA	432
Ala Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys	
130 135 140	
GAT TAT AAA AAT TCA CTT GCA AAA TTA AAA GAA GCG TAT AAA ATA GAT	480

Asp Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp
 145 150 155

GCG ACG ACA AGC CCT CAG AAT GTT TGG CTG GCA TAT GAA ACT TTG AAT 528
 Ala Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn
 160 165 170 175

TTA CAA AGC AAG CAA AAT AAC GCT CCA ACA TGG TGG AAT ACT GTA AAC 576
 Leu Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn
 180 185 190

AAA GAT CTA AAA CAA TTC TCT GAG AAA TAT TTA TGG ACC GCC TTG ACT 624
 Lys Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr
 195 200 205

TCT AAT GAT AAT CTT AGA AAG ATG TCA GGA GGT CGT ATG ATT AAC GAT 672
 Ser Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp
 210 215 220

ATA TTG AAC GAT ATC GAA AAC ATA AAG AAA GGA GAG GGA CAA CCG GGT 720
 Ile Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly
 225 230 235

GCT CCA GGA GGA AAG GAA AAC AAA TTA TCA GTG CTG ACC GTT CCT CAA 768
 Ala Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln
 240 245 250 255

GCT ATC TTA GCA GCA TTT GTT TCA GCA TTT GCT CCC GAA GGT ACA AAA 816
 Ala Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys
 260 265 270

ATT GAA AAT AAG GAC CTT GAT CCG TCT ACT TTA TAT CCT GGC CAA GGA 864
 Ile Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly
 275 280 285

GCA CTT CAC GTT ATT GAA CTA CAC CAA GAT AAG AGC GAT TGG AGC ATA 912
 Ala Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile
 290 295 300

AAA GTT CTC TAT AGA AAC AAT GAC CAA ATG AAG CTG AAA CCA ATG AAA 960
 Lys Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys
 305 310 315

CTT GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG 1008
 Leu Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met
 320 325 330 335

CTA CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA 1056
 Leu Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys
 340 345 350

ACG TCG TAAAAATTAA AAATAAAAC TTTCAATAT ATTTTCCGCT AAAATAAATA 1112
 Thr Ser

AATATGTTTG TATATTTAAA CTTATCAAAA TAATAGTAGT GTTTAATAA AGATTTAAA 1172

TAAATAATTG TAAAAAAAAA AAAAAAAA AAA 1205

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
1 5 10 15

Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
20 25 30

Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
35 40 45

Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
50 55 60

Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
65 70 75 80

Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
85 90 95

Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
100 105 110

Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
115 120 125

Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
130 135 140

Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala
145 150 155 160

Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu
165 170 175

Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys
180 185 190

Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
195 200 205

Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
210 215 220

Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala
225 230 235 240

Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
245 250 255

Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
260 265 270

Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
275 280 285

Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
290 295 300

Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
305 310 315 320

Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
325 330 335

Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
340 345 350

Ser

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TTTTTTTTTT TTTTTTTTTT TTACAATTAT TTATTTAAAA TCTTTATTAA AACACTACTA	60
TTATTTGAT AAGTTAAAT ATACAAACAT ATTTATTTAT TTTAGCGGAA AATATATTGA	120
AAAGTTTTTA TTTTTAATT TTACGACGTT TTACATAATT TATCATGAGC TTCTTCTCC	180
ATGTTATATT TTTGTAGCAT TGATTGAAA GTACCATAAG AACACTTGTC ACCGCATTGT	240
GCAAGTTCA TTGGTTTCAG CTTCATTTGG TCATTGTTTC TATAGAGAAC TTTTATGCTC	300
CAATCGCTCT TATCTTGGTG TAGTTCAATA ACGTGAAGTG CTCCTGGCC AGGATATAAA	360
GTAGACGGAT CAAGGTCCCTT ATTTCAATT TTTGTACCTT CGGGAGCAAA TGCTGAAACA	420
AATGCTGCTA AGATAGCTTG AGGAACGGTC ACCACTGATA ATTTGTTTTC CTTTCCTCCT	480
GGAGCACCCG GTTGTCCCTC TCCTTCTTT ATGTTTCGA TATCGTTCAA TATATCGTTA	540
ATCATAACGAC CTCCTGACAT CTTCTAAGA TTATCATTAG AAGTCAGGC GGTCCATAAA	600
TATTTCTCAG AGAATTGTT TAGATCTTG TTTACAGTAT TCCACCATGT TGGAGCGTTA	660
TTTGCTTGC TTTGTAATT CAAAGTTCA TATGCCAGCC AAACATTCTG AGGGCTTGTC	720
GTGCGATCTA TTTTATACGC TTCTTTAAT TTTGCAAGTG AATTTTATA ATCTTTGCA	780
CTTTTTGTTA ACAAGTCTCT TACTGCTATT TTCTGTTGTG CTATGAAGTT TGGACAAGTT	840
TTTGGACTAT AAAATTAGC ATATTCACCA AACGAAGAAA ATATGGTTT ATCTCCTTTC	900
TCTTTTGTC TAAACTGCCTT TTCTTTCT TCTAGACCAG AACCAATGAT AAGCGCTCCT	960
TCTTGAGATC TTCTCGTAGC ACTAGCTAAT GTCCAATAAT TTTTATTGAA ATCCCATTG	1020

TCAACTTTA AATTAGTTCT GTAAATGTTCG GATAATAATT TGCCAATTT TAATGCCTCT	1080
TCTTGACCTG CCGGTGTCAA TTGGCTTGAA TCTTCAGACT TGTGTGTAAT TTTTGGACCG	1140
CCTGGATAAT CACAAGGTGT ATGTGACATA CCTCGTGCAG TCGCAAACAC AAATTTCAAT	1200
TCTGC	1205

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA CCT Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro	48
1 5 10 15	
TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT TCA Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser	96
20 25 30	
AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC AAA Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys	144
35 40 45	
TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG GAT Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp	192
50 55 60	
TCA AAT AAA AAT TAT TGG ACA TTA GCT ACT GCT ACG AGA AGA TCT CAA Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln	240
65 70 75 80	
GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA GAA AAG GAA AAG GCA Glu Gly Ala Leu Ile Ile Ser Gly Leu Glu Glu Lys Ala	288
85 90 95	
GTT TGG ACA AAA GAG AAA GGA GAT AAA ACC ATA TTT TCT TCG TTT GGT Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly	336
100 105 110	
GAA TAT GCT AAA TTT TAT AGT CCA AAA ACT TGT CCA AAC TTC ATA GCA Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala	384
115 120 125	
CAA CAG AAA ATA GCA GTA AGA GAC TTG TTA ACA AAA AGT GCA AAA GAT Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp	432
130 135 140	

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro
1 5 10 15

Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser
20 25 30

Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys
35 40 45

Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp
50 55 60

Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln
65 70 75 80

Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala
85 90 95

Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly
100 105 110

Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala
115 120 125

Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp
130 135 140

Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala
145 150 155 160

Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu
165 170 175

Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys
180 185 190

Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser
195 200 205

Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile
210 215 220

Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala
225 230 235 240

Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala
245 250 255

Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile
260 265 270

Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala
275 280 285

Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys
290 295 300

Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu
305 310 315 320

Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu
325 330 335

Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr
340 345 350

Ser

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CGACGTTTA CATAATTAT CATGAGCTTC CTTCTCCATG TTATATTTT GTAGCATTGA 60
TTTGAAAGTA CCATAAGAAC ACTTGTCAACC GCATTGTGCA AGTTTCATTG GTTCAGCTT 120
CATTGGTCA TTGTTTCTAT AGAGAACTTT TATGCTCCAA TCGCTTTAT CTTGGTGTAG 180
TTCAATAACG TGAAGTGCTC CTTGGCCAGG ATATAAAGTA GACGGATCAA GGTCTTATT 240
TTCAATTCTT GTACCTTCGG GAGCAAATGC TGAAACAAAT GCTGCTAAGA TAGCTTGAGG 300
AACGGTCAGC ACTGATAATT TGTTTCCTT TCCTCCTGGA GCACCCGGTT GTCCCTCTCC 360
TTTCTTATG TTTTCGATAT CGTTCAATAT ATCGTTAACATC ATACGACCTC CTGACATCTT 420
TCTAAGATTA TCATTAGAAG TCAAGGCGGT CCATAAAATAT TTCTCAGAGA ATTGTTTAG 480
ATCTTTGTTT ACAGTATTCC ACCATGTTGG AGCGTTATTT TGCTTGCTTT GTAAATTCAA 540
AGTTTCATAT GCCAGCCAAA CATTCTGAGG GCTTGTGTC GCATCTATTT TATACGCTTC 600
TTTTAATTTC GCAAGTGAAT TTTTATAATC TTTTGCACCTT TTTGTTAACAGTCTCTTAC 660
TGCTATTTTC TGTTGTGCTA TGAAGTTGG ACAAGTTTT GGACTATAAA ATTTAGCATA 720
TTCACCAAAC GAAGAAAATA TGGTTTATC TCCTTCTCT TTTGTCACAA CTGCCTTTTC 780
CTTTCTTCT AGACCAGAAC CAATGATAAG CGCTCCTTCT TGAGATCTTC TCGTAGCACT 840
AGCTAATGTC CAATAATTTC TATTGAAATC CCATTTGTCA ACTTTAAAT TAGTTCTGTA 900
ATGTTCGGAT AATAATTGCA CAATTTTAA TGCCTCTTCT TGACCTGCCG GTGTCAATTG 960
GCTTGAATCT TCAGACTTGT GTGTAATTTC TGGACCGCCT GGATAATCAC AAGGTGTATG 1020

TGACATACCT CGTGCAGTCG CAAACACAAA TTTCAATTC

1059

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Xaa = any amino acid
 - (B) LOCATION: 1
- (ix) FEATURE:
 - (A) NAME/KEY: Xaa = any amino acid
 - (B) LOCATION: 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Xaa Glu Leu Lys Phe Val Phe Val Met Val Lys Gly Pro Asp His Glu
1 5 10 15
Ala Cys Asn Tyr Ala Gly Gly Xaa Gln
20 25

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATG GTT AAA GGT CCA GAT CAC GAA GCT TGT AAC TAT GCA GGA GGT CCT 48
Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro
1 5 10 15
CAG TTA ACT ACT CTT CAA GAA AAA GAT AGT GTT CTA ACT GAA GAT GGC 96
Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly
20 25 30
AAG ACA GAA GCA TAC GAA TTG GGA AAA CTT TTG GAC AAG GTA TAT AAA 144
Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys
35 40 45
AAA CAA TTA AAA GTT GAC AAA TGG GAT GCC ACG AAA ACC TAC TGG GCT 192
Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala
50 55 60

GTG TCC ACA AAA GCT ATG CGT ACT AAA GAA GCA GCC TTA ATT GTA GGA	240
Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly	
65 70 75 80	
GCA GGA TTG GAA AAT AAT CCT GCA AAA GCT AAA GGT AAT TGG ACA CAA	288
Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln	
85 90 95	
CAA CAG CTC GAT TCA ACA CAT TTT GAT GCG ATG CCT GGC TTT TCT AGA	336
Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg	
100 105 110	
TTT TGG AAT CCT CAA CAA TGT CCG GCA TAT TTC AGA GCG CTC TCG CTA	384
Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu	
115 120 125	
CAA AAT CAG AAA ATA AAG AAA T	406
Gln Asn Gln Lys Ile Lys Lys	
130 135	

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro	
1 5 10 15	
Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly	
20 25 30	
Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys	
35 40 45	
Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala	
50 55 60	
Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly	
65 70 75 80	
Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln	
85 90 95	
Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg	
100 105 110	
Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu	
115 120 125	
Gln Asn Gln Lys Ile Lys Lys	
130 135	

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (Genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTTCTTTAT TTTCTGATTG TGTAGCGAGA GCGCTCTGAA ATATGCCGGA CATTGTTGAG	60
GATTCCAAAA TCTAGAAAAG CCAGGCATCG CATCAAAATG TGTTGAATCG AGCTGTTGTT	120
GTGTCCAATT ACCTTTAGCT TTTGCAGGAT TATTTTCCAA TCCTGCTCCT ACAATTAAGG	180
CTGCTTCTTT AGTACCGATA GCTTTTGTGG ACACAGCCCA GTAGGTTTTC GTGGCATCCC	240
ATTTGTCAAC TTTTAATTGT TTTTTATATA CCTTGTCCAA AAGTTTCCC AATTCTGTATG	300
CTTCTGTCTT GCCATCTTCA GTTAGAACAC TATCTTTTC TTGAAGAGTA GTTAACGTAG	360
GACCTCCTGC ATAGTTACAA GCTTCGTGAT CTGGACCTTT AACCAT	406

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GAA GTT ATG GAT AAA TTG CGA AAA CAG GCA CCT CCT AAA ACT GAT GGC	48
Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly	
1 5 10 15	
AAT CCT CCA AAA ACA ACC ATA ATG AGT ACA CTT CAA AAG CAA CAA ATA	96
Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile	
20 25 30	
AGT TGC ACA GAA GTG AAA GCG GTT AAC TTA GAA AGT CAT GTT TGT GCT	144
Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala	
35 40 45	
TAT GAT TGT AGT CAA CCT GAA ACT GCA GGA ATT ACA TGC AAA GGA AAT	192
Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn	
50 55 60	
AAG TGT GAT TGT CCT AAA AAA CGC TAAAAATTAA TTCAAAACAT TTACATTTT	246
Lys Cys Asp Cys Pro Lys Lys Arg	
65 70	

TATTAATATT CAACTATCAA AAATTCTGTG TTGATTGTTA TTATATTAT CATACTTACT	306
AGAAATAAAA TTTTATAACA TTGTTAACAT GAAATTGAAT ACACATAATA TTATAATTAG	366
TGAGGTTAAA AGAAATAAAC CGAATATCCA AATCAAAAAA AAAAAAAA AAAA	420

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly	
1 5 10 15	

Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile	
20 25 30	

Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala	
35 40 45	

Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn	
50 55 60	

Lys Cys Asp Cys Pro Lys Lys Arg	
65 70	

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTTTTTTTTT TTTTTTTT GATTGGATA TTCGGTTAT TTCTTTAAC CTCACTAATT	60
ATAATATTAT GTGTATTCAA TTTCGAATTA ACAATGTTAT AAAATTTAT TTCTAGTAAC	120
TATGATAAAAT ATAATAACAA TCAACACAGA ATTTTGATA GTTGAATATT AATAAAAAT	180
GTAAAATGTT TGAATAAATT TTTAGCGTTT TTTAGGACAA TCACACTTAT TTCCCTTGCA	240
TGTAATTCCCT GCAGTTTCAG GTTGACTACA ATCATAAGCA CAAACATGAC TTTCTAAGTT	300
AACCGCTTTC ACTTCTGTGC AACTTATTTG TTGCTTTGA AGTGTACTCA TTATGGTTGT	360
TTTTGGAGGA TTGCCATCAG TTTTAGGAGG TGCCTGTTT CGCAATTAT CCATAACTTC	420

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser
1 5 10 15

Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe
20 25 30

Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys
35 40 45

Gly Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr Arg Pro Asn
50 55 60

Gln Lys His Cys Tyr Cys Glu
65 70

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asn Asp Lys Leu Gln Phe Val Phe Val Met Ala Arg Gly Pro Asp His
1 5 10 15

Glu Ala Cys Asn Tyr Pro Gly Gly Pro
20 25

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGTGGATCCG TCAAAATGG TCACTG

26

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCGGAATTCTG GTTATTGCA ATAACAGT

28

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..54
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GCGCGGATCC GCATATGGAA GACATCTGGA AAGTTAATAA AAAATGTACA TCAG

54

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..45
 - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCGGAATTCT TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCC

45

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..46
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AAATTGTWT TTGTWATGGT WAAAGGWCCW GATCATGAAG C

41

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..37
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATGAACCGWG GWAATACWCG WAARATHAS

29

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

1000231202 02020202
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAAGT WATGG AYAAAT TRAG RCARGC

26

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Tyr Phe Asn Lys Leu Val Gln Ser Trp Thr Glu Pro Met Val Phe Lys
1 5 10 15

Tyr Pro Tyr

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTAATACGAC TCACTATATA GGGC

24